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Cryptococcus Neoformans and Other Opportunistic *Cryptococcus* Species in Pigeon Dropping in Saudi Arabia: Identification and Characterization by DNA Sequencing

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Abstract

The prevalent variants of *Cryptococcus neoformans*, and other Cryptococcus species in pigeon excreta in Western Region of Saudi Arabia. Ninety pigeon dropping samples were directly in Niger Seed agar, and suspected colonies sequenced using Illumina MiSeq. Species identification was determined using sequence reads mapping to a reference genomes of the two C. neoformans variants. In addition, sequence reads were identified using KmerFinder tool. Internal Transcribed Spacer 2 in the rDNA was also used for fungal barcoding of none Cryptococcus neoformans species using two fungal identification databases. Phylogeny was studied using CSI Phylogeny (Center for Genomic Epidemiology, Denmark). The Cryptococcus neoformans var. grubii mitochondrion and chromosome 1 reference sequences (accession number NC_004336.1 and CP022321.1, respectively) were used for sequences comparison and variants calling. Fifteen Cryptococcus isolates were obtained, 11 were identified as Cryptococcus neoformans variety grubii and 4 were found to be other opportunistic *cryptococcus* species. Phylogeny analysis of Cryptococcus neoformans variety grubii isolates showed high degree of similarity between the Cryptococcus neoformans isolates especially at the mitochondrial genome level. This study supports the fact that pathogenic and opportunistic Cryptococcus species are prevalent in domestic bird excreta which is an easy source of infection in susceptible population.

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